
Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2009; month=9; day=18; hr=9; min=2; sec=8; ms=325;]

Reviewer Comments:

1.

E355 Empty lines found between the amino acid numbering and the proteins SEQID (16)

E321 No. of Bases conflict, this line has no nucleotides SEQID (16) POS (496)

<210> 16

<211> 497

<212> PRT

<213> Pan troglodytes

* * * * * * * * *

Gln

29

The Sequence Listing file must end at the bottom of the last SEQ ID #. There can be no extra information following the last SEQ ID # in the file. Please remove extra information, "29", found at the end of the file, after SEQ ID # 16.

2.

W213 Artificial or Unknown found in <213> in SEQ ID (15)

The warnings shown above are ok and require no response.

Validated By CRFValidator v 1.0.3

Application No: 10552287 Version No: 4.0

Input Set:

Output Set:

Started: 2009-08-14 14:12:34.463 **Finished:** 2009-08-14 14:12:35.639

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 176 ms

Total Warnings: 1
Total Errors: 2

No. of SeqIDs Defined: 16

Actual SeqID Count: 16

Err	or code	Error Description
W	213	Artificial or Unknown found in <213> in SEQ ID (15)
E	355	Empty lines found between the amino acid numbering and the
E	321	No of Bases conflict, this line has no nucleotides SEOID (16)

SEQUENCE LISTING

<110> Futerman, Anthony Sussman, Joel Silman, Israel Harel, Michal Dvir, Hay Toker, Lilly Swetlana Adamsky <120> GAUCHER DISEASE DRUGS AND METHODS OF IDENTIFYING SAME <130> 30227 <140> 10552287 <141> 2007-01-04 <160> 16 <170> PatentIn version 3.2 <210> 1 <211> 497 <212> PRT <213> Homo sapiens <400> 1 Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys 5 10 Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro 20 25 30 Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg 35 40 45 Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly 60 50 55 Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly 65 70 75 80 Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu 85 90

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe

Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
100 105 110

115 120 125

Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu 130 135 140 His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu 145 150 155 Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala 165 170 175 Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn 180 185 190 Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr 195 200 205 Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys 210 215 220 Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu 225 230 235 240 Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln 245 250 Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr 265 260 270 His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu 275 280 285 Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr 290 295 300 Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala 305 310 315 320 Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu 330 325

Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val

345

350

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile 360 Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala 375 380 Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser 390 395 400 385 Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met 405 410 415 Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln 420 425 430 Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala 440 445 435 Leu Met Asn Pro Asp Gly Ser Ala Val Val Val Leu Asn Arg Ser 450 455 460 Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu 470 475 480 465 Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg 485 490 495 Gln <210> 2 <211> 497 <212> PRT <213> Homo sapiens <220> <221> misc_feature <222> (370)..(370) <223> Asn to Ser mutant <400> 2

Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys

10

Val	Суз	Asn	Ala 20	Thr	Tyr	Cys	Asp	Ser 25	Phe	Asp	Pro	Pro	Thr 30	Phe	Pro
Ala	Leu	Gly 35	Thr	Phe	Ser	Arg	Tyr 40	Glu	Ser	Thr	Arg	Ser 45	Gly	Arg	Arg
Met	Glu 50	Leu	Ser	Met	Gly	Pro 55	Ile	Gln	Ala	Asn	His 60	Thr	Gly	Thr	Gly
Leu 65	Leu	Leu	Thr	Leu	Gln 70	Pro	Glu	Gln	Lys	Phe 75	Gln	Lys	Val	Lys	Gly 80
Phe	Gly	Gly	Ala	Met 85	Thr	Asp	Ala	Ala	Ala 90	Leu	Asn	Ile	Leu	Ala 95	Leu
Ser	Pro	Pro	Ala 100	Gln	Asn	Leu	Leu	Leu 105	Lys	Ser	Tyr	Phe	Ser 110	Glu	Glu
Gly	Ile	Gly 115	Tyr	Asn	Ile	Ile	Arg 120	Val	Pro	Met	Ala	Ser 125	Суз	Asp	Phe
Ser	Ile 130	Arg	Thr	Tyr	Thr	Tyr 135	Ala	Asp	Thr	Pro	Asp 140	Asp	Phe	Gln	Leu
His 145	Asn	Phe	Ser	Leu	Pro 150	Glu	Glu	Asp	Thr	Lys 155	Leu	Lys	Ile	Pro	Leu 160
Ile	His	Arg	Ala	Leu 165	Gln	Leu	Ala	Gln	Arg 170	Pro	Val	Ser	Leu	Leu 175	Ala
Ser	Pro	Trp	Thr 180	Ser	Pro	Thr	Trp	Leu 185	Lys	Thr	Asn	Gly	Ala 190	Val	Asn
Gly	Lys	Gly 195	Ser	Leu	Lys	Gly	Gln 200	Pro	Gly	Asp	Ile	Tyr 205	His	Gln	Thr
Trp	Ala 210	Arg	Tyr	Phe	Val	Lys 215	Phe	Leu	Asp	Ala	Tyr 220	Ala	Glu	His	Lys
Leu 225	Gln	Phe	Trp	Ala	Val 230	Thr	Ala	Glu	Asn	Glu 235	Pro	Ser	Ala	Gly	Leu 240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro	o Glu His Gln 255
Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala 260 265	a Asn Ser Thr 270
His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg 275 280 285	=
Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala 290 295 300	a Ala Lys Tyr
Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu 305 310 315	ı Ala Pro Ala 320
Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Ass 325 330	n Thr Met Leu 335
Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu 340 345	u Gln Ser Val 350
Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His	
Thr Ser Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp 370 375 380	o Asn Leu Ala
Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe 385 390 395	e Val Asp Ser 400
Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys 405 410	G Gln Pro Met 415
Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu 420 425	ı Gly Ser Gln 430
Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp 435 440 445	
Leu Met Asn Pro Asp Gly Ser Ala Val Val Val Leu 450 455 460	ı Asn Arg Ser

Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu 465 470 475 480 Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg 485 490 Gln <210> 3 <211> 497 <212> PRT <213> Homo sapiens <220> <221> misc_feature <222> (394)..(394) <223> Val to Leu mutant <400> 3 Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys 1 5 10 Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro 20 25 30 Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg 35 40 45 Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly 50 55 60 Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly 65 70 75 80 Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu 95 85 90 Ser Pro Pro Ala Gln Asn Leu Leu Lys Ser Tyr Phe Ser Glu Glu 100 105 110

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe

115 120 125

Ser	Ile 130	Arg	Thr	Tyr	Thr	Tyr 135	Ala	Asp	Thr	Pro	Asp 140	Asp	Phe	Gln	Leu
His 145	Asn	Phe	Ser	Leu	Pro 150	Glu	Glu	Asp	Thr	Lys 155	Leu	Lys	Ile	Pro	Leu 160
Ile	His	Arg	Ala	Leu 165	Gln	Leu	Ala	Gln	Arg 170	Pro	Val	Ser	Leu	Leu 175	Ala
Ser	Pro	Trp	Thr 180	Ser	Pro	Thr	Trp	Leu 185	Lys	Thr	Asn	Gly	Ala 190	Val	Asn
		195			_		200					205		Gln	
	210					215					220			His	
225					230					235				Gly	240
				245			-		250					His 255 Ser	
			260					265					270	Leu	
		275					280					285		Lys	
	290			_		295					300			Pro	
305					310					315				Met	320
_				325					330					335 Ser	
2.110		201	340		-10		- ± y	345	-10	2110	1	Jiu	350	201	. 41

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile

355 360 365

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala 370 375 380

Leu Asn Pro Glu Gly Gly Pro Asn Trp Leu Arg Asn Phe Val Asp Ser 385 390 395 400

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met \$405\$

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln 420 425 430

Arg Val Gly Leu Val Ala Ser Gln Lys As
n Asp Leu Asp Ala Val Ala 435 440445

Leu Met Asn Pro Asp Gly Ser Ala Val Val Val Leu Asn Arg Ser 450 455 460

Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu 465 470 475 489

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg 485 490 495

Gln

<210> 4

<211> 497

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<222> (409)..(409)

<223> Asp to His mutant

<400> 4

Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys 1 5 10 15

Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro

20 25 30

Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg 35 40 45 Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly 55 Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Leu Asn Ile Leu Ala Leu 85 90 95 Ser Pro Pro Ala Gln Asn Leu Leu Lys Ser Tyr Phe Ser Glu Glu 100 105 110 Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe 115 120 125 Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu 135 140 130 His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu 150 155 160 145 Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala 170 165 175 Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn 180 185 190 Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr 195 200 205

250

255

Arg Asp		le Ala	ı Arg	Asp	Leu	Gly 265	Pro	Thr	Leu	Ala	Asn 270	Ser	Thr
His His	Asn V 275	al Arç	, Leu	Leu	Met 280	Leu	Asp	Asp	Gln	Arg 285	Leu	Leu	Leu
Pro His 290	Trp A	la Lys	: Val	Val 295	Leu	Thr	Asp	Pro	Glu 300	Ala	Ala	Lys	Tyr
Val His 305	Gly I	le Ala	310	His	Trp	Tyr	Leu	Asp 315	Phe	Leu	Ala	Pro	Ala 320
Lys Ala	Thr L	eu Gly 325		Thr	His	Arg	Leu 330	Phe	Pro	Asn	Thr	Met 335	Leu
Phe Ala		ilu Ala 40	ı Cys	Val	Gly	Ser 345	Lys	Phe	Trp	Glu	Gln 350	Ser	Val
Arg Leu	Gly S 355	er Trp	Asp	Arg	Gly 360	Met	Gln	Tyr	Ser	His 365	Ser	Ile	Ile
Thr Asn 370	Leu L	eu Tyı	His	Val 375	Val	Gly	Trp	Thr	Asp 380	Trp	Asn	Leu	Ala
Leu Asn 385	Pro G	ilu Gly	Gly 390	Pro	Asn	Trp	Val	Arg 395	Asn	Phe	Val	Asp	Ser 400
Pro Ile	Ile V	al Asr 405		Thr	Lys	His	Thr 410	Phe	Tyr	Lys	Gln	Pro 415	Met
Phe Tyr		eu Gly 20	His	Phe	Ser	Lys 425	Phe	Ile	Pro	Glu	Gly 430	Ser	Gln
Arg Val	Gly L 435	eu Val	. Ala	Ser	Gln 440	Lys	Asn	Asp	Leu	Asp 445	Ala	Val	Ala
Leu Met 450	Asn P	ro Asp	Gly	Ser 455	Ala	Val	Val	Val	Val 460	Leu	Asn	Arg	Ser
Ser Lys 465	Asp V	al Pro	170 Leu	Thr	Ile	Lys	Asp	Pro 475	Ala	Val	Gly	Phe	Leu 480

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg \$485\$